#### SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: Ryals, John

Friedrich, Leslie Uknes, Scott Molina, Antonio Ruess, Wilhelm

Knauf-Beiter, Gertrude

Kung, Ruth Kessmann, Helmut Oostendorp, Michael

- (ii) TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
- (iii) NUMBER OF SEQUENCES: 32
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Novartis Corporation
    - (B) STREET: 3054 Cornwallis Road
    - (C) CITY: Research Triangle Park
    - (D) STATE: North Carolina
    - (E) COUNTRY: USA (F) ZIP: 27709

    - (v) COMPUTER READABLE FORM:
      - (A) MEDIUM TYPE: Floppy disk
      - (B) COMPUTER: IBM PC compatible
      - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER:
    - (B) FILING DATE:
    - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/761,543
  - (B) FILING DATE: 6-DEC-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/034,378
  - (B) FILING DATE: 27-DEC-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/034,379
  - (B) FILING DATE: 27-DEC-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/034,382
  - (B) FILING DATE: 27-DEC-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/034,730
  - (B) FILING DATE: 10-JAN-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/035,021
  - (B) FILING DATE: 10-JAN-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/035,022

- (B) FILING DATE: 10-JAN-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/035,024
  - (B) FILING DATE: 10-JAN-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/875,015
  - (B) FILING DATE: 16-JUL-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Meigs, J. Timothy
  - (B) REGISTRATION NUMBER: 38,241
  - (C) REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (919) 541-8587
    - (B) TELEFAX: (919) 541-8689
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5655 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION: 2787..3347
    - (D) OTHER INFORMATION: /product= "1st exon of NIM1"
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION: 3427..4162
    - (D) OTHER INFORMATION: /product= "2nd exon of NIM1"
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION: 4271..4474
    - (D) OTHER INFORMATION: /product= "3rd exon of NIM1"
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION: 4586..4866
    - (D) OTHER INFORMATION: /product= "4th exon of NIM1"
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATAGTCTTCA	AACCAACCAC	TAAACAGTAT	CAGGTCATAC	CAAAGCCAGA	AGTGAAGGGT	120
TGGGATATGT	CATTGGGTTT	AGCGGTAATC	GGATTGAACC	CTTTCCGGTA	TAAAATACAA	180
AGGCTTTCGC	AGTCTCGGCG	TATGTGTATG	TCTCGGGGTA	TCTACCATTT	GAATCACAGA	240
ACTTTTATGT	GCGAAGTTTT	CGATTCTGAT	TCGTTTACCT	GGAAGAGATT	AGAAAATTTG	300
CGTCTACCAA	AAACAGACAG	ATTAATTTT	TCCAACCCGA	TACAAGTTTC	GGGGTTCTTG	360
CATTGGATAT	CACGGAACAA	CAATGTGATC	CGGTTTTGTC	TCAAAACCGA	AACTTGGTCC	420
TTCTTCCATA	CTCCGAACTC	TGATGTTTTC	TCAGGATTAG	TCAGATACGA	AGGGAAGCTA	480
GGTGCTATTC	GTCAGTGGAC	AAACAAAGAT	CAAGAAGATG	TTCACGAGTT	ATGGGTTTTA	540
AAGAGCAGTT	TTGAAAAGTC	GTGGGTTAAA	GTGAAAGATA	TTAAAAGCAT	TGGAGTAGAT	600
TTGATTACGT	GGACTCCAAG	CAACGACGTT	GTATTGTTTC	GTAGTAGTGA	TCGTGGTTGC	660
CTCTACAACA	TAAACGCAGA	GAAGTTGAAT	TTAGTTTATG	CAAAAAAAGA	GGGATCTGAT	720
TGTTCTTTCG	TTTGTTTTCC	GTTTTGTTCT	GATTACGAGA	GGGTTGATCT	GAACGGAAGA	780
AGCAACGGGC	CGACACTTTA	AAAAAAAAT	AAAAAAAATG	GGCCGACAAA	TGCAAACGTA	840
GTTGACAAGG	ATCTCAAGTC	TCAAGTCTCA	ATTGGCTCGC	TCATTGTGGG	GCATAAATAT	900
ATCTAGTGAT	GTTTAATTGT	TTTTTATAAG	GTAAAAAGGA	ATATTGAATT	TTGTTTCTTA	960
GGTTTATGTA	АТААТАССАА	ACATTGTTTT	ATGAATATTT	AATCTGATTT	TTTGGCTAGT	1020
TATTTTATTA	TATCAAGGGT	TCCTGTTTAT	AGTTGAAAAC	AGTTACTGTA	TAGAAAATAG	1080
TGTCCCAATT	TTCTCTCTTA	AATAATATAT	TAGTTAATAA	AAGATATTTT	AATATATTAG	1140
ATATACATAA	TATCTAAAGC	AACACATATT	TAGACACAAC	ACGTAATATC	TTACTATTGT	1200
TTACATATAT	TTATAGCTTA	CCAATATAAC	CCGTATCTAT	GTTTTATAAG	CTTTTATACA	1260
ATATATGTAC	GGTATGCTGT	CCACGTATAT	ATATTCTCCA	AAAAAAACGC	ATGGTACACA	1320
AAATTTATTA	AATATTTGGC	AATTGGGTGT	TTATCTAAAG	TTTATCACAA	TATTTATCAA	1380
CTATAATAGA	TGGTAGAAGA	TAAAAAAATT	ATATCAGATT	GATTCAATTA	AATTTTATAA	1440
TATATCATTI	TAAAAAATTA	ATTAAAAGAA	. AACTATTTCA	. TAAAATTGTT	' CAAAAGATAA	1500
TTAGTAAAAT	TAATTAAATA	TGTGATGCTA	TTGAGTTATA	GAGAGTTATI	GTAAATTTAC	1560
TTAAAATCAT	ACAAATCTTA	TCCTAATTTA	ACTTATCATT	' TAAGAAATAC	: AAAAGTAAAA	1620
AACGCGGAAA	A GCAATAATTI	ATTTACCTTA	TTATAACTCC	TATATAAAGT	ACTCTGTTTA	1680
TTCAACATAA	A TCTTACGTTG	G TTGTATTCAT	AGGCATCTTT	AACCTATCTT	TTCATTTTCT	1740
GATCTCGATC	C GTTTTCGATC	CAACAAAATG	AGTCTACCGG	TGAGGAACCA	AGAGGTGATT	1800
ATGCAGATTO	CTTCTTCTTC	TCAGTTTCCA	GCAACATCGA	GTCCGGAAAA	A CACCAATCAA	1860
GTGAAGGAT	G AGCCAAATTI	GTTTAGACG1	GTTATGAAT1	TGCTTTTAC	G TCGTAGTTAT	1920
TGAAAAAGC	r GATTTATCGO	C ATGATTCAGA	A ACGAGAAGTT	GAAGGCAAAT	T AACTAAAGAA	1980

GTCTTTTATA TO	GTATACAAT A	ATTGTTTTT	AAATCAAAT	C CTAATTAAA	A AAATA	PATTC 2040
ATTATGACTT TO	CATGTTTTT A	ATGTAATTT	ATTCCTATA	AT CTATAATGA	TTTGT	rgrga 2100
AGAGCGTTTT C	ATTTGCTAT A	GAACAAGGA	GAATAGTTO	CC AGGAAATAT	T CGACT	TGATT 2160
TAATTATAGT G	TAAACATGC T	GAACACTGA	AAATTACTT	TT TTCAATAAA	C GAAAA	ATATA 2220
ATATACATTA C	AAAACTTAT G	TGAATAAAG	CATGAAACT	TT AATATACG	T CCCTT	PATCA 2280
TTTTACTTCA A	AGAAAATAA A	CAGAAATGT	AACTTTCAC	CA TGTAAATCI	TA ATTCT	TAAAT 2340
TTAAAAAATA A	ТАТТТАТАТ А	TTTATATGA	AAATAACGA	AA CCGGATGA	AATAA	ATTTT 2400
ATATATTTAT A	TCATCTCCA A	ATCTAGTTT	GGTTCAGG	GG CTTACCGA	AC CGGAT"	rgaac 2460
TTCTCATATA C	AAAAATTAG C	AACACAAAA	TGTCTCCG	GT ATAAATAC	ra acatt	TATAA 2520
CCCGAACCGG T	TTAGCTTCC T	GTTATATCT	TTTTAAAAA	AA GATCTCTGA	AC AAAGA	TTCCT 2580
TTCCTGGAAA T	TTACCGGTT T	TGGTGAAAT	GTAAACCG'	TG GGACGAGG	AT GCTTC	TTCAT 2640
ATCTCACCAC C	ACTCTCGTT G	ACTTGACTT	GGCTCTGC	TC GTCAATGG	TT ATCTT	CGATC 2700
TTTAACCAAA T	CCAGTTGAT A	AGGTCTCTT	CGTTGATT	AG CAGAGATC	C TTTAA	TTTGT 2760
GAATTTCAAT T	CATCGGAAC C	TGTTG ATG Met 1	Asp Thr	ACC ATT GAT Thr Ile Asp 5	GGA TTC Gly Phe	GCC 2813 Ala
GAT TCT TAT Asp Ser Tyr 10	GAA ATC AGO Glu Ile Ser 15	Ser Thr	Ser Phe V	TC GCT ACC ( al Ala Thr 2 20	GAT AAC Asp Asn	ACC 2861 Thr 25
GAC TCC TCT Asp Ser Ser	ATT GTT TAT Ile Val Tyr 30	CTG GCC Leu Ala	GCC GAA C. Ala Glu G 35	AA GTA CTC . ln Val Leu	ACC GGA Thr Gly 40	CCT 2909 Pro
GAT GTA TCT Asp Val Ser	GCT CTG CAA Ala Leu Glr 45	TTG CTC	TCC AAC A Ser Asn S 50	GC TTC GAA er Phe Glu	TCC GTC Ser Val 55	TTT 2957 Phe
GAC TCG CCG Asp Ser Pro 60	Asp Asp Phe	Tvr Ser	Asp Ala L	AG CTT GTT ys Leu Val 70	Leu Ser	GAC 3005 Asp
GGC CGG GAA Gly Arg Glu 75	GTT TCT TTC Val Ser Phe	C CAC CGG His Arg 80	TGC GTT T Cys Val L	TG TCA GCG eu Ser Ala 85	AGA AGC Arg Ser	TCT 3053 Ser
TTC TTC AAG Phe Phe Lys 90	AGC GCT TTA Ser Ala Let 99	ı Ala Ala	Ala Lys L	AG GAG AAA ys Glu Lys .00	GAC TCC Asp Ser	AAC 3101 Asn 105
AAC ACC GCC Asn Thr Ala	GCC GTG AAG Ala Val Ly: 110	G CTC GAG S Leu Glu	CTT AAG G Leu Lys G 115	SAG ATT GCC Slu Ile Ala	AAG GAT Lys Asp 120	TAC 3149 Tyr
GAA GTC GGT Glu Val Gly	TTC GAT TCC Phe Asp Se: 125	G GTT GTG Val Val	ACT GTT T Thr Val I 130	TTG GCT TAT Leu Ala Tyr	GTT TAC Val Tyr 135	AGC 3197 Ser
AGC AGA GTG Ser Arg Val 140	AGA CCG CCG Arg Pro Pro	G CCT AAA o Pro Lys 145	GGA GTT T Gly Val S	GCT GAA TGC Ser Glu Cys 150	GCA GAC Ala Asp	GAG 3245 Glu

AAT TGC TGC Asn Cys Cys 155	CAC GTG GC' His Val Ala	TGC CGG Cys Arg 160	CCG GCG Pro Ala	GTG GAT Val Asp 165	TTC ATG Phe Met	TTG GAG Leu Glu	3293
GTT CTC TAT Val Leu Tyr 170	TTG GCT TT Leu Ala Ph 17	e Ile Phe	AAG ATC Lys Ile	CCT GAA Pro Glu 180	TTA ATT Leu Ile	ACT CTC Thr Leu 185	3341
TAT CAG GTAA Tyr Gln	AACACC ATC	rgcatta a	GCTATGGT	T ACACAT	rcat gaat	'ATGTTC	3397
TTACTTGAGT A	CTTGTATTT	GTATTTCAG			GAC GTT Asp Val		3450
AAA GTT GTT Lys Val Val	ATA GAG GA Ile Glu As 200	C ACA TTG p Thr Leu	GTT ATA Val Ile 205	Leu Lys	CTT GCT Leu Ala	AAT ATA Asn Ile 210	3498
TGT GGT AAA Cys Gly Lys	GCT TGT AT Ala Cys Me 215	G AAG CTA t Lys Leu	TTG GAT Leu Asp 220	AGA TGT Arg Cys	AAA GAG Lys Glu 225	ATT ATT Ile Ile	3546
GTC AAG TCT Val Lys Ser 230	AAT GTA GA Asn Val As	T ATG GTT p Met Val 235	Ser Leu	GAA AAG Glu Lys	TCA TTG Ser Leu 240	CCG GAA Pro Glu	3594
GAG CTT GTT Glu Leu Val 245	AAA GAG AT Lys Glu Il	A ATT GAT e Ile Asp 250	AGA CGT Arg Arg	AAA GAG Lys Glu 255	Leu Gly	TTG GAG Leu Glu	3642
GTA CCT AAA Val Pro Lys 260	GTA AAG AA Val Lys Ly 26	s His Val	TCG AAT Ser Asr	GTA CAT Val His 270	AAG GCA Lys Ala	CTT GAC Leu Asp 275	3690
TCG GAT GAT Ser Asp Asp	ATT GAG TT Ile Glu Le 280	A GTC AAG u Val Lys	TTG CTI Leu Leu 285	ı Leu Lys	GAG GAT Glu Asp	CAC ACC His Thr 290	3738
AAT CTA GAT Asn Leu Asp	GAT GCG TO Asp Ala Cy 295	T GCT CTT s Ala Leu	CAT TTO His Phe 300	C GCT GTT e Ala Val	GCA TAT Ala Tyr 305	TGC AAT Cys Asn	3786
GTG AAG ACC Val Lys Thr 310	GCA ACA GA Ala Thr As	T CTT TTA p Leu Leu 315	ı Lys Leı	r GAT CTI ı Asp Leu	GCC GAT Ala Asp 320	GTC AAC Val Asn	3834
CAT AGG AAT His Arg Asn 325	CCG AGG GC Pro Arg G	GA TAT ACC y Tyr Thi 330	GTG CT	r CAT GTT 1 His Val 335	Ala Ala	ATG CGG Met Arg	3882
AAG GAG CCA Lys Glu Pro 340	Gln Leu I	TA CTA TCT Le Leu Sei 15	CTA TTO	G GAA AAA u Glu Lys 350	A GGT GCA s Gly Ala	AGT GCA Ser Ala 355	3930
TCA GAA GCA Ser Glu Ala	ACT TTG G Thr Leu G 360	AA GGT AGA Lu Gly Arq	A ACC GC Thr Ala 36	a Leu Met	G ATC GCA Ile Ala	AAA CAA Lys Gln 370	3978
GCC ACT ATG Ala Thr Met	GCG GTT G Ala Val G 375	AA TGT AA lu Cys Ası	T AAT AT n Asn Il 380	C CCG GAO e Pro Gli	G CAA TGC 1 Gln Cys 385	Lys His	4026

TCT CTC AAA GGC CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys 390 395 400	4074
CGA GAA CAA ATT CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCC GCC Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala 405 410 415	4122
GAT GAA TTG AAG ATG ACG CTG CTC GAT CTT GAA AAT AGA G Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg 420 430	4162
GTATCTATCA AGTCTTATTT CTTATATGTT TGAATTAAAT TTATGTCCTC TCTATTAGGA	4222
AACTGAGTGA ACTAATGATA ACTATTCTTT GTGTCGTCCA CTGTTTAG TT GCA CTT Val Ala Leu 435	4278
GCT CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala 440 445 450	4326
GAA ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp 455 460 465	4374
CGT CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro 470 475 480	4422
TTC AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys 485 490 495	4470
ACC G GTATGGATTC TCACCCACTT CATCGGACTC CTTATCACAA AAAACAAAAC	4524
Thr	4524 4584
Thr 500	
Thr 500  TAAATGATCT TTAAACATGG TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA  G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu	4584
Thr 500  TAAATGATCT TTAAACATGG TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA  G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu 505  GAC CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu	4584 4629
Thr 500  TAAATGATCT TTAAACATGG TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA  G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu 505 510 515  GAC CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu 520 525 530  GAC GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu	4584 4629 4677
Thr 500  TAAATGATCT TTAAACATGG TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA  G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu 505 510 515  GAC CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu 520 530  GAC GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu 535 545  ATA CAA GAG ACA CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asp Leu Glu Leu	4584 4629 4677 4725
Thr 500  TAAATGATCT TTAAACATGG TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA  G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC  Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu  505  GAC CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA  Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu  520  GAC GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA  Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu  535  ATA CAA GAG ACA CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA  Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu  550  GGA AAT TCG TCC CTG ACA GAT TCG ACT TCT TCC ACA TCG AAA TCA ACC  Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr	4584 4629 4677 4725

TAACTGTTTA	TGTCTATCGT	TGGCGTCATA	TAGTTTCGCT	CTTCGTTTTG	CATCCTGTGT	4986
ATTATTGCTG	CAGGTGTGCT	TCAAACAAAT	GTTGTAACAA	TTTGAACCAA	TGGTATACAG	5046
ATTTGTAATA	TATATTTATG	TACATCAACA	ATAACCCATG	ATGGTGTTAC	AGAGTTGCTA	5106
GAATCAAAGT	GTGAAATAAT	GTCAAATTGT	TCATCTGTTG	GATATTTTCC	ACCAAGAACC	5166
AAAAGAATAT	TCAAGTTCCC	TGAACTTCTG	GCAACATTCA	TGTTATATGT	ATCTTCCTAA	5226
TTCTTCCTTT	AACCTTTTGT	AACTCGAATT	ACACAGCAAG	TTAGTTTCAG	GTCTAGAGAT	5286
AAGAGAACAC	TGAGTGGGCG	TGTAAGGTGC	ATTCTCCTAG	TCAGCTCCAT	TGCATCCAAC	5346
ATTTGTGAAT	GACACAAGTT	AACAATCCTT	TGCACCATTT	CTGGGTGCAT	ACATGGAAAC	5406
TTCTTCGATT	GAAACTTCCC	ACATGTGCAG	GTGCGTTCGC	TGTCACTGAT	AGACCAAGAG	5466
ACTGAAAGCT	TTCACAAATT	GCCCTCAAAT	CTTCTGTTTC	TATCGTCATG	ACTCCATATC	5526
TCCGACCACT	GGTCATGAGC	CAGAGCCCAC	TGATTTTGAG	GGAATTGGGC	TAACCATTTC	5586
CGAGCTTCTG	AGTCCTTCTT	TTTGATGTCC	TTTATGTAGG	AATCAAATTC	TTCCTTCTGA	5646
CTTGTGGAT						5655

### (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 594 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser 1 10 15

Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu 20 25 30

Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu
35 40 45

Leu Ser Asn Ser Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr 50 55 60

Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His 65 70 75 80

Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala 85 90 95

Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu 100 105 110

Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val 115 120 125

Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro 130 135 140

Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp 180 Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu 280 Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala 295 Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala 310 Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala 325 Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile 360 Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln 395 390 Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala 485 490 495

Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser 500 505 510

Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala 515 520 525

Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg 530 540

Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn 545 550 555 560

Leu Glu Leu Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser 565 570 575

Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg 580 585 590

Arg \*

- (2) INFORMATION FOR SEQ ID NO:3:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Phe Gln Pro Ala Gly His Gly Gln Asp Trp Ala Met Glu Gly Pro 1 5 10 15

Arg Asp Gly Leu Lys Lys Glu Arg Leu Val Asp Asp Arg His Asp Ser 20 25 30

Gly Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu 35 40 45

Leu Arg Glu Ile Arg Leu Gln Pro Gln Glu Ala Pro Leu Ala Ala Glu 50 60

Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu 65 70 75 80

Ala Ile Ile His Glu Glu Lys Pro Leu Thr Met Glu Val Ile Gly Gln
85 90 95

Val Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln Gln 100 105 110

Thr Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Gly Ile Ala Glu 115 120 125

Ala Leu Leu Lys Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly 130 135 140

Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val 145 150 155 160

Ala Val Leu Thr Gln Thr Cys Thr Pro Gln His Leu His Ser Val Leu 165 170 175

Gln Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Thr 180 185 190

His Gly Tyr Leu Ala Ile Val Glu His Leu Val Thr Leu Gly Ala Asp  $195 \hspace{1.5cm} 200 \hspace{1.5cm} 205$ 

Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala 210 215 220

Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly 225 230 235 240

Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu 245 250 255

Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu 260 265 270

Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser 275 280 285

Tyr Asp Thr Glu Ser Glu Phe Thr Glu Asp Glu Leu Pro Tyr Asp Asp 290 295 300

Cys Val Phe Gly Gly Gln Arg Leu Thr Leu 305

### (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 314 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln Pro Ala Gly His Gly Gln Asp Trp Ala Met Glu Gly Pro 1 5 10 15

Arg Asp Gly Leu Lys Lys Glu Arg Leu Val Asp Asp Arg His Asp Ser 20 25 30

Gly Leu Asp Ser Met Lys Asp Glu Asp Tyr Glu Gln Met Val Lys Glu 35 40 45

Leu Arg Glu Ile Arg Leu Gln Pro Gln Glu Ala Pro Leu Ala Ala Glu 50 55 60

Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu 65 70 75 80

Ala Ile Ile His Glu Glu Lys Thr Leu Thr Met Glu Val Ile Gly Gln 85 90 95

Val Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln Gln 100 105 110

Thr Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Gly Ile Ala Glu 115 120 125

Ala Leu Leu Lys Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly 130 140

Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val 145 150 155 160

Ala Val Leu Thr Gln Thr Cys Thr Pro Gln His Leu His Ser Val Leu 165 170 175

Gln Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Ile 180 185 190

His Gly Tyr Leu Gly Ile Val Glu His Leu Val Thr Leu Gly Ala Asp 195 200 205

Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala 210 215 220

Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly 225 230 235 240

Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu 245 250 255

Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu 260 265 270

Thr Leu Glu Asn Leu Gln Thr Leu Pro Glu Ser Glu Asp Glu Glu Ser 275 280 285

Tyr Asp Thr Glu Ser Glu Phe Thr Glu Asp Glu Leu Pro Tyr Asp Asp 290 295 300

Cys Val Phe Gly Gly Gln Arg Leu Thr Leu 305

### (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 314 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Phe Gln Pro Ala Glu Pro Gly Gln Glu Trp Ala Met Glu Gly Pro 1 5 10 15

Arg Asp Ala Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His Asp Ser

20 25 30

Gly Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu 35 40 45

Leu Arg Glu Ile Arg Leu Glu Pro Gln Glu Ala Pro Arg Gly Ala Glu

Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu

Ala Ile Ile His Glu Glu Lys Ala Leu Thr Met Glu Val Val Arg Gln

Val Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln Gln 100 105 110

Thr Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Glu Ile Ala Glu 115 120 125

Ala Leu Leu Glu Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly 130 135 140

Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val 145 150 155 160

Gly Val Leu Thr Gln Pro Arg Gly Thr Gln His Leu His Ser Ile Leu 165 170 175

Gln Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Ile 180 185 190

His Gly Tyr Leu Gly Ile Val Glu Leu Leu Val Ser Leu Gly Ala Asp 195 200 205

Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala 210 215 220

Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly 225 230 240

Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu 245 250 255

Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Leu Gly Gln Leu 260 265 270

Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser 275 280 285

Tyr Asp Thr Glu Ser Glu Phe Thr Glu Asp Glu Leu Pro Tyr Asp Asp 290 295 300

Cys Val Leu Gly Gly Gln Arg Leu Thr Leu 305 310

### (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2011 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
- (ix) FEATURE:

  - (A) NAME/KEY: misc\_feature
    (B) LOCATION: 1..2011
    (D) OTHER INFORMATION: /note= "NIM1 cDNA sequence"
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 43..1824
  - (D) OTHER INFORMATION: /product= "NIM1 protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TG ATG GAC ACC ACC Met Asp Thr Thr 1													
ATT GAT GGA TTC GCC GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val 5	102												
GCT ACC GAT AAC ACC GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln 25 30	150												
GTA CTC ACC GGA CCT GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser 40 45 50	198												
TTC GAA TCC GTC TTT GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys 55 60 65	246												
CTT GTT CTC TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu 70 75 80	294												
TCA GCG AGA AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys 85 90 95 100	342												
GAG AAA GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu 105	390												
ATT GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu 120 125 130	438												
GCT TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser 135 140 145	486												
GAA TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val 150	534												
GAT TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro 165 170 175 180	582												

GAA Glu	TTA Leu	ATT Ile	ACT Thr	CTC Leu 185	TAT Tyr	CAG G1n	AGG Arg	CAC His	TTA Leu 190	TTG Leu	GAC Asp	GTT Val	GTA Val	GAC Asp 195	AAA Lys	630
GTT Val	GTT Val	ATA Ile	GAG Glu 200	GAC Asp	ACA Thr	TTG Leu	GTT Val	ATA Ile 205	CTC Leu	AAG Lys	CTT Leu	GCT Ala	AAT Asn 210	ATA Ile	TGT Cys	678
GGT Gly	AAA Lys	GCT Ala 215	TGT Cys	ATG Met	AAG Lys	CTA Leu	TTG Leu 220	GAT Asp	AGA Arg	TGT Cys	AAA Lys	GAG Glu 225	ATT Ile	ATT Ile	GTC Val	726
AAG Lys	TCT Ser 230	AAT Asn	GTA Val	GAT Asp	ATG Met	GTT Val 235	AGT Ser	CTT Leu	GAA Glu	AAG Lys	TCA Ser 240	TTG Leu	CCG Pro	GAA Glu	GAG Glu	774
CTT Leu 245	GTT Val	AAA Lys	GAG Glu	ATA Ile	ATT Ile 250	GAT Asp	AGA Arg	CGT Arg	AAA Lys	GAG Glu 255	CTT Leu	GGT Gly	TTG Leu	GAG Glu	GTA Val 260	822
CCT Pro	AAA Lys	GTA Val	AAG Lys	AAA Lys 265	CAT His	GTC Val	TCG Ser	AAT Asn	GTA Val 270	CAT His	AAG Lys	GCA Ala	CTT Leu	GAC Asp 275	TCG Ser	870
GAT Asp	GAT Asp	ATT Ile	GAG Glu 280	TTA Leu	GTC Val	AAG Lys	TTG Leu	CTT Leu 285	TTG Leu	AAA Lys	GAG Glu	GAT Asp	CAC His 290	ACC Thr	AAT Asn	918
CTA Leu	GAT Asp	GAT Asp 295	GCG Ala	TGT Cys	GCT Ala	CTT Leu	CAT His 300	TTC Phe	GCT Ala	GTT Val	GCA Ala	TAT Tyr 305	TGC Cys	AAT Asn	GTG Val	966
AAG Lys	ACC Thr 310	GCA Ala	ACA Thr	GAT Asp	CTT Leu	TTA Leu 315	AAA Lys	CTT Leu	GAT Asp	CTT Leu	GCC Ala 320	GAT Asp	GTC Val	AAC Asn	CAT His	1014
AGG Arg 325	AAT Asn	CCG Pro	AGG Arg	GGA Gly	TAT Tyr 330	ACG Thr	GTG Val	CTT Leu	CAT His	GTT Val 335	GCT Ala	GCG Ala	ATG Met	CGG Arg	AAG Lys 340	1062
GAG Glu	CCA Pro	CAA G1n	TTG Leu	ATA Ile 345	CTA Leu	TCT Ser	CTA Leu	TTG Leu	GAA Glu 350	AAA Lys	GGT Gly	GCA Ala	AGT Ser	GCA Ala 355	TCA Ser	1110
GAA Glu	GCA Ala	ACT Thr	TTG Leu 360	GAA Glu	GGT Gly	AGA Arg	ACC Thr	GCA Ala 365	Leu	ATG Met	ATC Ile	GCA Ala	AAA Lys 370	CAA Gln	GCC Ala	1158
ACT Thr	ATG Met	GCG Ala 375	Val	GAA Glu	TGT Cys	AAT Asn	AAT Asn 380	Ile	CCG Pro	GAG Glu	CAA Gln	TGC Cys 385	Lys	CAT	TCT Ser	1206
CTC Leu	AAA Lys 390	Gly	CGA Arg	CTA Leu	TGT Cys	GTA Val 395	Glu	ATA Ile	CTA Leu	GAG Glu	CAA Gln 400	Glu	GAC Asp	AAA Lys	. CGA Arg	1254
GAA Glu 405	Gln	ATT Ile	CCT Pro	AGA Arg	GAT Asp 410	Val	CCT Pro	CCC Pro	TCT Ser	TTT Phe 415	Ala	GTG Val	GCG Ala	GCC Ala	GAT Asp 420	1302
GAA Glu	TTG Leu	AAG Lys	ATG Met	ACG Thr 425	Leu	CTC	GAT Asp	CTT Leu	GAA Glu 430	Asn	AGA Arg	GTI Val	GCA Ala	CTT Lev 435	GCT Ala	1350

CAA Gln	CGT Arg	CTT Leu	TTT Phe 440	CCA Pro	ACG Thr	GAA Glu	GCA Ala	CAA Gln 445	GCT Ala	GCA Ala	ATG Met	GAG Glu	ATC Ile 450	GCC Ala	GAA Glu	1398
ATG Met	AAG Lys	GGA Gly 455	ACA Thr	TGT Cys	GAG Glu	TTC Phe	ATA Ile 460	GTG Val	ACT Thr	AGC Ser	CTC Leu	GAG Glu 465	CCT Pro	GAC Asp	CGT Arg	1446
CTC Leu	ACT Thr 470	GGT Gly	ACG Thr	AAG Lys	AGA Arg	ACA Thr 475	TCA Ser	CCG Pro	GGT Gly	GTA Val	AAG Lys 480	ATA Ile	GCA Ala	CCT Pro	TTC Phe	1494
AGA Arg 485	ATC Ile	CTA Leu	GAA Glu	GAG Glu	CAT His 490	CAA Gln	AGT Ser	AGA Arg	CTA Leu	AAA Lys 495	GCG Ala	CTT Leu	TCT Ser	AAA Lys	ACC Thr 500	1542
GTG Val	GAA Glu	CTC Leu	GGG Gly	AAA Lys 505	CGA Arg	TTC Phe	TTC Phe	CCG Pro	CGC Arg 510	TGT Cys	TCG Ser	GCA Ala	GTG Val	CTC Leu 515	GAC Asp	1590
CAG Gln	ATT Ile	ATG Met	AAC Asn 520	Cys	GAG Glu	GAC Asp	TTG Leu	ACT Thr 525	CAA Gln	CTG Leu	GCT Ala	TGC Cys	GGA Gly 530	GAA Glu	GAC Asp	1638
GAC Asp	ACT Thr	GCT Ala 535	GAG Glu	AAA Lys	CGA Arg	CTA Leu	CAA Gln 540	AAG Lys	AAG Lys	CAA Gln	AGG Arg	TAC Tyr 545	ATG Met	GAA Glu	ATA Ile	1686
CAA Gln	GAG Glu 550	ACA Thr	CTA Leu	AAG Lys	AAG Lys	GCC Ala 555	TTT Phe	AGT Ser	GAG Glu	GAC Asp	AAT Asn 560	TTG Leu	GAA Glu	TTA Leu	GGA Gly	1734
AAT Asn 565	TTG Leu	TCC Ser	CTG Leu	ACA Thr	GAT Asp 570	TCG Ser	ACT Thr	TCT Ser	TCC Ser	ACA Thr 575	TCG Ser	AAA Lys	TCA Ser	ACC Thr	GGT Gly 580	1782
GGA Gly	AAG Lys	AGG Arg	TCT Ser	AAC Asn 585	CGT Arg	AAA Lys	CTC Leu	TCT Ser	CAT His 590	CGT Arg	CGT Arg	CGG Arg	TGA *			1824
GAC'	TCTT	GCC	TCTT	AGTG	TA A'	$\operatorname{TTTT}$	TGCT	G TA	CCAT	ATAA	TTC	TGTT	TTC	ATGA	TGACTG	1884
TAA	CTGT	TTA	TGTC	TATC	GT T	GGCG	TCAT	а та	GTTT	CGCT	CTT	CGTT	TTG	CATC	CTGTGT	1944
ATT.	ATTG	CTG	CAGG	TGTG	CT T	CAAA	CAAA	T GT	TGTA	ACAA	TTT	GAAC	CAA	TGGT	ATACAG	2004
ATT	TGTA															2011

### (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2011 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

  - (A) NAME/KEY: CDS
    (B) LOCATION: 43..1824
- (D) OTHER INFORMATION: /product= "altered form of NIM1" /note= "Serine residues at amino acid positions 55 and 59 in

wild-type NIM1 gene product have been changed to Alanine residues."

### (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 205..217

(D) OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TG ATG GAC ACC ACC Met Asp Thr Thr	54											
ATT GAT GGA TTC GCC GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val 5 20	102											
GCT ACC GAT AAC ACC GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln 25 30 35	150											
GTA CTC ACC GGA CCT GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser 40 45 50	198											
TTC GAA GCC GTC TTT GAC GCG CCG GAT GAT TTC TAC AGC GAC GCT AAG Phe Glu Ala Val Phe Asp Ala Pro Asp Asp Phe Tyr Ser Asp Ala Lys 55 60 65	246											
CTT GTT CTC TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu 70 75 80	294											
TCA GCG AGA AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys 85 90 95 100	342											
GAG AAA GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu 105 110 115	390											
ATT GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG  Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu  120 125 130	438											
GCT TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser 135 140 145	486											
GAA TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val 150 155 160	534											
GAT TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro 165 170 175 180	582											
GAA TTA ATT ACT CTC TAT CAG AGG CAC TTA TTG GAC GTT GTA GAC AAA Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys  185 190 195	630											
GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA TGT	678											

Val	Val	Ile	Glu 200	Asp	Thr	Leu	Val	Ile 205	Leu	Lys	Leu	Ala	Asn 210	Ile	Cys	
GGT Gly	AAA Lys	GCT Ala 215	TGT	ATG Met	AAG Lys	CTA Leu	TTG Leu 220	GAT Asp	AGA Arg	TGT Cys	AAA Lys	GAG Glu 225	ATT Ile	ATT Ile	GTC Val	726
AAG Lys	TCT Ser 230	AAT Asn	GTA Val	GAT Asp	ATG Met	GTT Val 235	AGT Ser	CTT Leu	GAA Glu	AAG Lys	TCA Ser 240	TTG Leu	CCG Pro	GAA Glu	GAG Glu	774
CTT Leu 245	GTT Val	AAA Lys	GAG Glu	ATA Ile	ATT Ile 250	GAT Asp	AGA Arg	CGT Arg	AAA Lys	GAG Glu 255	CTT Leu	GGT Gly	TTG Leu	GAG Glu	GTA Val 260	822
CCT Pro	AAA Lys	GTA Val	AAG Lys	AAA Lys 265	CAT His	GTC Val	TCG Ser	AAT Asn	GTA Val 270	CAT His	AAG Lys	GCA Ala	CTT Leu	GAC Asp 275	TCG Ser	870
GAT Asp	GAT Asp	ATT Ile	GAG Glu 280	TTA Leu	GTC Val	AAG Lys	TTG Leu	CTT Leu 285	TTG Leu	AAA Lys	GAG Glu	GAT Asp	CAC His 290	ACC Thr	AAT Asn	918
CTA Leu	GAT Asp	GAT Asp 295	GCG Ala	TGT Cys	GCT Ala	CTT Leu	CAT His 300	TTC Phe	GCT Ala	GTT Val	GCA Ala	TAT Tyr 305	TGC Cys	AAT Asn	GTG Val	966
AAG Lys	ACC Thr 310	GCA Ala	ACA Thr	GAT Asp	CTT Leu	TTA Leu 315	AAA Lys	CTT Leu	GAT Asp	CTT Leu	GCC Ala 320	GAT Asp	GTC Val	AAC Asn	CAT His	1014
AGG Arg 325	AAT Asn	CCG Pro	AGG Arg	GGA Gly	TAT Tyr 330	ACG Thr	GTG Val	CTT Leu	CAT His	GTT Val 335	GCT Ala	GCG Ala	ATG Met	CGG Arg	AAG Lys 340	1062
GAG Glu	CCA Pro	CAA Gln	TTG Leu	ATA Ile 345	CTA Leu	TCT Ser	CTA Leu	TTG Leu	GAA Glu 350	AAA Lys	GGT Gly	GCA Ala	AGT Ser	GCA Ala 355	TCA Ser	1110
GAA Glu	GCA Ala	ACT Thr	TTG Leu 360	GAA Glu	GGT Gly	AGA Arg	ACC Thr	GCA Ala 365		ATG Met	ATC Ile	GCA Ala	AAA Lys 370	CAA Gln	GCC Ala	1158
ACT Thr	ATG Met	GCG Ala 375	Val	GAA Glu	TGT Cys	AAT Asn	AAT Asn 380	ATC Ile	CCG Pro	GAG Glu	CAA Gln	TGC Cys 385	Lys	CAT His	TCT Ser	1206
CTC Leu	AAA Lys 390	Gly	CGA Arg	CTA Leu	TGT Cys	GTA Val 395	GAA Glu	ATA Ile	CTA Leu	GAG Glu	CAA Gln 400	Glu	GAC Asp	AAA Lys	CGA Arg	1254
GAA Glu 405	Gln	ATT Ile	CCT Pro	AGA Arg	GAT Asp 410	GTT Val	CCT Pro	CCC	TCT Ser	TTT Phe 415	Ala	. GTG Val	GCG Ala	GCC Ala	GAT Asp 420	1302
GAA Glu	TTG Leu	AAG Lys	ATG Met	ACG Thr 425	Leu	CTC Leu	GAT Asp	CTT	GAA Glu 430	. Asn	AGA Arg	GTT Val	GCA Ala	CTT Leu 435	GCT Ala	1350
CAA Gln	. CGT . Arg	CTT Leu	TTT Phe 440	Pro	ACG Thr	GAA Glu	GCA Ala	CAZ Glr 445	ı Ala	GCA Ala	ATG Met	GAG Glu	ATC Ile 450	: Ala	GAA Glu	1398
ATG Met	AAG Lys	GGA Gly	A ACA	TGT Cys	GAG Glu	TTC Phe	: ATA	GTO Val	ACT Thr	AGC Ser	CTC	GAG Glu	CCT	GAC Asp	CGT Arg	1446

ATTTGTA

460 465 455 CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT TTC 1494 Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe 470 475 AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA ACC 1542 Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr 490 495 GTG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC GAC 1590 Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp 505 CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA GAC 1638 Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp 530 525 520 GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA ATA 1686 Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile 540 535 CAA GAG ACA CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA GGA 1734 Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly 555 AAT TTG TCC CTG ACA GAT TCG ACT TCT TCC ACA TCG AAA TCA ACC GGT 1782 Asn Leu Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr Gly 570 GGA AAG AGG TCT AAC CGT AAA CTC TCT CAT CGT CGG TGA 1824 Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg Arg \* 585 GACTCTTGCC TCTTAGTGTA ATTTTTGCTG TACCATATAA TTCTGTTTTC ATGATGACTG 1884 TAACTGTTTA TGTCTATCGT TGGCGTCATA TAGTTTCGCT CTTCGTTTTG CATCCTGTGT 1944

2004

2011

#### (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 594 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser 1 5 10 15

ATTATTGCTG CAGGTGTGCT TCAAACAAAT GTTGTAACAA TTTGAACCAA TGGTATACAG

Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu 20 25 30

Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu
35
40
45

Leu Ser Asn Ser Phe Glu Ala Val Phe Asp Ala Pro Asp Asp Phe Tyr 50 55 60

Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro 135 Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp 185 Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu 200 Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser 230 Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu 245 Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala 295 Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala 315 Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln 380 Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala 405 410 415

Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg 420 425 430

Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Met 435 440 445

Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu 450 455 460

Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys 465 470 475 480

Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala 485 490 495

Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser 500 510

Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala 515 520 525

Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg 530 540

Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn 545 550 555

Leu Glu Leu Gly Asn Leu Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser 565 570 575

Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg 580 585 590

Arg \*

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1597 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..1410
  - (D) OTHER INFORMATION: /product= "Altered form of NIM1" /note= "N-terminal deletion compared to wild-type NIM1 sequence."
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GAT TCG GTT GTG ACT GTT TTG GCT TAT GTT TAC AGC AGC AGA GTG
Met Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val

1 10 15

AGA CCG CCG CCT AAA GGA GTT TCT GAA TGC GCA GAC GAG AAT TGC TGC Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys 48

96

25 30 20 CAC GTG GCT TGC CGG CCG GCG GTG GAT TTC ATG TTG GAG GTT CTC TAT 144 His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr 40 35 TTG GCT TTC ATC TTC AAG ATC CCT GAA TTA ATT ACT CTC TAT CAG AGG 192 Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg 55 CAC TTA TTG GAC GTT GTA GAC AAA GTT GTT ATA GAG GAC ACA TTG GTT 240 His Leu Leu Asp Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val ATA CTC AAG CTT GCT AAT ATA TGT GGT AAA GCT TGT ATG AAG CTA TTG 288 Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu GAT AGA TGT AAA GAG ATT ATT GTC AAG TCT AAT GTA GAT ATG GTT AGT 336 Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser CTT GAA AAG TCA TTG CCG GAA GAG CTT GTT AAA GAG ATA ATT GAT AGA 384 Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg CGT AAA GAG CTT GGT TTG GAG GTA CCT AAA GTA AAG AAA CAT GTC TCG 432 Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser 135 AAT GTA CAT AAG GCA CTT GAC TCG GAT GAT ATT GAG TTA GTC AAG TTG 480 Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu 150 CTT TTG AAA GAG GAT CAC ACC AAT CTA GAT GAT GCG TGT GCT CTT CAT 528 Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His 165 TTC GCT GTT GCA TAT TGC AAT GTG AAG ACC GCA ACA GAT CTT TTA AAA 576 Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys 624 CTT GAT CTT GCC GAT GTC AAC CAT AGG AAT CCG AGG GGA TAT ACG GTG Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val 195 CTT CAT GTT GCT GCG ATG CGG AAG GAG CCA CAA TTG ATA CTA TCT CTA 672 Leu His Val Ala Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu 210 TTG GAA AAA GGT GCA AGT GCA TCA GAA GCA ACT TTG GAA GGT AGA ACC 720 Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr 230 225 GCA CTC ATG ATC GCA AAA CAA GCC ACT ATG GCG GTT GAA TGT AAT AAT 768 Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn 250 ATC CCG GAG CAA TGC AAG CAT TCT CTC AAA GGC CGA CTA TGT GTA GAA 816 Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu 864 ATA CTA GAG CAA GAA GAC AAA CGA GAA CAA ATT CCT AGA GAT GTT CCT Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro

280

275

CCC TCT TTT GCA GTG GCG GCC GAT GAA TTG AAG ATG ACG CTG CTC GAT Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp 290 295 300	912
CTT GAA AAT AGA GTT GCA CTT GCT CAA CGT CTT TTT CCA ACG GAA GCA Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala 305 310 320	960
CAA GCT GCA ATG GAG ATC GCC GAA ATG AAG GGA ACA TGT GAG TTC ATA Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile 325 330 335	1008
GTG ACT AGC CTC GAG CCT GAC CGT CTC ACT GGT ACG AAG AGA ACA TCA Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser 340 345 350	1056
CCG GGT GTA AAG ATA GCA CCT TTC AGA ATC CTA GAA GAG CAT CAA AGT Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser 355 360 365	1104
AGA CTA AAA GCG CTT TCT AAA ACC GTG GAA CTC GGG AAA CGA TTC TTC Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe 370 380	1152
CCG CGC TGT TCG GCA GTG CTC GAC CAG ATT ATG AAC TGT GAG GAC TTG Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu 385 390 395 400	1200
ACT CAA CTG GCT TGC GGA GAA GAC GAC ACT GCT GAG AAA CGA CTA CAA Thr Gln Leu Ala Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln 405 410 415	1248
AAG AAG CAA AGG TAC ATG GAA ATA CAA GAG ACA CTA AAG AAG GCC TTT Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe 420 425 430	1296
AGT GAG GAC AAT TTG GAA TTA GGA AAT TTG TCC CTG ACA GAT TCG ACT Ser Glu Asp Asn Leu Glu Leu Gly Asn Leu Ser Leu Thr Asp Ser Thr 435 440 445	1344
TCT TCC ACA TCG AAA TCA ACC GGT GGA AAG AGG TCT AAC CGT AAA CTC Ser Ser Thr Ser Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu 450 455 460	1392
TCT CAT CGT CGG TGA GACTCTTGCC TCTTAGTGTA ATTTTTGCTG Ser His Arg Arg * 470	1440
TACCATATAA TTCTGTTTTC ATGATGACTG TAACTGTTTA TGTCTATCGT TGGCGTCATA	1500
TAGTTTCGCT CTTCGTTTTG CATCCTGTGT ATTATTGCTG CAGGTGTGCT TCAAACAAAT	1560
GTTGTAACAA TTTGAACCAA TGGTATACAG ATTTGTA	1597

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 470 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser 135 Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu 215 Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu 265 Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala 315 310 Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile

Val	Thr	Ser	Leu 340	Glu	Pro	Asp	Arg	Leu 345	Thr	Gly	Thr	Lys	Arg 350	Thr	Ser	
Pro	Gly	Val 355	Lys	Ile	Ala	Pro	Phe 360	Arg	Ile	Leu	Glu	Glu 365	His	Gln	Ser	
Arg	Leu 370	Lys	Ala	Leu	Ser	Lys 375	Thr	Val	Glu	Leu	Gly 380	Lys	Arg	Phe	Phe	
Pro 385	Arg	Cys	Ser	Ala	Val 390	Leu	Asp	Gln	Ile	Met 395	Asn	Cys	Glu	Asp	Leu 400	
Thr	Gln	Leu	Ala	Cys 405	Gly	Glu	Asp	Asp	Thr 410	Ala	Glu	Lys	Arg	Leu 415	Gln	
Lys	Lys	Gln	Arg 420	Tyr	Met	Glu	Ile	Gln 425	Glu	Thr	Leu	Lys	Lys 430	Ala	Phe	
Ser	Glu	Asp 435	Asn	Leu	Glu	Leu	Gly 440	Asn	Leu	Ser	Leu	Thr 445	Asp	Ser	Thr	
Ser	Ser 450	Thr	Ser	Lys	Ser	Thr 455	Gly	Gly	Lys	Arg	Ser 460	Asn	Arg	Lys	Leu	
Ser 465	His	Arg	Arg	Arg	* 470											
(2)	INF	ORMA'	TION	FOR	SEQ	ID :	NO:1	1:								
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 1608 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>															
	(11	) MO:	LIECU.	UL 1	IF15.	CDN	A									
,	(ix note	( (	A) N. B) L D) O	AME/ OCAT THER	ION: INF	43. ORMA	TION	: /p	rodu red	ct= to w	"Alt ild-	ered type	for NIM	m of 1."	NIM1"	
(x:	i) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0:11	:						
GA?	PCTCT	TTA	ATTT	GTGA	AT T	TCAA	TTCA	T CG	GAAC	CTGT	TG	ATG Met 1	GAC Asp	ACC Thr	ACC Thr	54
Ile	r GAT e Asp 5	' GGA Gly	TTC Phe	GCC Ala	GAT Asp 10	Ser	TAT Tyr	GAA Glu	ATC Ile	AGC Ser 15	Ser	ACT Thr	AGT Ser	TTC Phe	GTC Val 20	102
GC'	T ACC a Thr	GAT Asp	' AAC Asn	ACC Thr 25	Asp	TCC Ser	TCT Ser	`ATT	GTT Val	Tyr	CTG Leu	GCC Ala	GCC Ala	GAA Glu 35	. Gln	150
GT: Va	A CTO	ACC Thr	GGA Gly 40	Pro	GAT Asp	GTA Val	TCT Ser	GCT Ala 45	Lev	CAA Gln	TTG Lev	G CTC	TCC Ser 50	Asn	AGC Ser	198
TT Ph	C GAA	TCC Ser	GTC Val	TTT Phe	GAC Asp	TCG Ser	CCG Pro	GAT Asp	GAT Asp	TTC Phe	TAC Tyr	AGC Ser	C GAC	GCT Ala	AAG Lys	246

60 55 CTT GTT CTC TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG 294 Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu TCA GCG AGA AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG 342 Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Lys Lys 85 390 GAG AAA GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu 110 105 ATT GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG 438 Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu 125 486 GCT TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Lys Gly Val Ser GAA TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG 534 Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val 582 GAT TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro 170 GAA TTA ATT ACT CTC TAT CAG AGG CAC TTA TTG GAC GTT GTA GAC AAA 630 Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys 185 190 GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA TGT 678 Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys 200 GGT AAA GCT TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT GTC 726 Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val 215 AAG TCT AAT GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA GAG 774 Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu 235 230 CTT GTT AAA GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG GTA 822 Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val 245 CCT AAA GTA AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC TCG 870 Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser 265 GAT GAT ATT GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC AAT 918 Asp Asp Ile Glu Leu Val Lys Leu Leu Lys Glu Asp His Thr Asn CTA GAT GAT GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT GTG 966 Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val 300 1014 AAG ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC CAT Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His 320 315

65

AGG Arg 325	AAT Asn	CCG Pro	AGG Arg	GGA Gly	TAT Tyr 330	ACG Thr	GTG Val	CTT Leu	CAT His	GTT Val 335	GCT Ala	GCG Ala	ATG Met	CGG Arg	AAG Lys 340	Í	1062
GAG Glu	CCA Pro	CAA Gln	TTG Leu	ATA Ile 345	CTA Leu	TCT Ser	CTA Leu	TTG Leu	GAA Glu 350	AAA Lys	GGT Gly	GCA Ala	AGT Ser	GCA Ala 355	TCA Ser	:	1110
GAA Glu	GCA Ala	ACT Thr	TTG Leu 360	GAA Glu	GGT Gly	AGA Arg	ACC Thr	GCA Ala 365	CTC Leu	ATG Met	ATC Ile	GCA Ala	AAA Lys 370	CAA Gln	GCC Ala	:	1158
ACT Thr	ATG Met	GCG Ala 375	GTT Val	GAA Glu	TGT Cys	AAT Asn	AAT Asn 380	ATC Ile	CCG Pro	GAG Glu	CAA Gln	TGC Cys 385	AAG Lys	CAT His	TCT Ser		1206
CTC Leu	AAA Lys 390	GGC Gly	CGA Arg	CTA Leu	TGT Cys	GTA Val 395	GAA Glu	ATA Ile	CTA Leu	GAG Glu	CAA Gln 400	GAA Glu	GAC Asp	AAA Lys	CGA Arg		1254
GAA Glu 405	CAA Gln	ATT Ile	CCT Pro	AGA Arg	GAT Asp 410	GTT Val	CCT Pro	CCC Pro	TCT Ser	TTT Phe 415	GCA Ala	GTG Val	GCG Ala	GCC Ala	GAT Asp 420		1302
GAA Glu	TTG Leu	AAG Lys	ATG Met	ACG Thr 425	CTG Leu	CTC Leu	GAT Asp	CTT Leu	GAA Glu 430	AAT Asn	AGA Arg	GTT Val	GCA Ala	CTT Leu 435	GCT Ala		1350
CAA Gln	CGT Arg	CTT Leu	TTT Phe 440	CCA Pro	ACG Thr	GAA Glu	GCA Ala	CAA Gln 445	GCT Ala	GCA Ala	ATG Met	GAG Glu	ATC Ile 450	GCC Ala	GAA Glu		1398
ATG Met	AAG Lys	GGA Gly 455	ACA Thr	TGT Cys	GAG Glu	TTC Phe	ATA Ile 460	GTG Val	ACT Thr	AGC Ser	CTC Leu	GAG Glu 465	CCT Pro	GAC Asp	CGT Arg		1446
					AGA Arg												1494
					CAT His 490												1542
					CGA Arg					Cys					GAC Asp		1590
	ATT Ile			Cys	TGA *												1608

### (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 522 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu 105 Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp 185 Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser 235 Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala 315 Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly 345 340

Ala	Ser	Ala 355	Ser	Glu	Ala	Thr	Leu 360	Glu	Gly	Arg	Thr	Ala 365	Leu	Met	Ile	
Ala	Lys 370	Gln	Ala	Thr	Met	Ala 375	Val	Glu	Cys	Asn	Asn 380	Ile	Pro	Glu	Gln	
Cys 385	Lys	His	Ser	Leu	Lys 390	Gly	Arg	Leu	Cys	Val 395	Glu	Ile	Leu	Glu	Gln 400	
Glu	Asp	Lys	Arg	Glu 405	Gln	Ile	Pro	Arg	Asp 410	Val	Pro	Pro	Ser	Phe 415	Ala	
Val	Ala	Ala	Asp 420	Glu	Leu	Lys	Met	Thr 425	Leu	Leu	Asp	Leu	Glu 430	Asn	Arg	
Val	Ala	Leu 435	Ala	Gln	Arg	Leu	Phe 440	Pro	Thr	Glu	Ala	Gln 445	Ala	Ala	Met	
Glu	Ile 450	Ala	Glu	Met	Lys	Gly 455	Thr	Cys	Glu	Phe	Ile 460	Val	Thr	Ser	Leu	
Glu 465	Pro	Asp	Arg	Leu	Thr 470	Gly	Thr	Lys	Arg	Thr 475	Ser	Pro	Gly	Val	Lys 480	
Ile	Ala	Pro	Phe	Arg 485	Ile	Leu	Glu	Glu	His 490	Gln	Ser	Arg	Leu	Lys 495	Ala	
Leu	Ser	Lys	Thr 500	Val	Glu	Leu	Gly	Lys 505	Arg	Phe	Phe	Pro	Arg 510	Cys	Ser	
Ala	Val	Leu 515	Asp	Gln	Ile	Met	Asn 520	Cys	*							
(2)	INF	ORMA'	TION	FOR	SEQ	ID I	NO:1	3:								
	(2) INFORMATION FOR SEQ ID NO:13:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 1194 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear															
	(ii	) MO	LECU	LE T	YPE:	CDN	A									
/	<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 11194     (D) OTHER INFORMATION: /product= "Altered form of NIM1" /note= "N-terminal/C-terminal chimera."</pre>															
(xi	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0:13	:						
	Asp				Thr					Val					GTG Val	48
AGA Arg	CCG Pro	CCG Pro	CCT Pro 20	Lys	GGA Gly	GTT Val	TCT Ser	GAA Glu 25	Сув	GCA Ala	GAC Asp	GAG Glu	AAT Asn 30	Cys	TGC Cys	96
			Cys										. Val		TAT Tyr	144

TTG Leu	GCT Ala 50	TTC Phe	ATC Ile	TTC Phe	AAG Lys	ATC Ile 55	CCT Pro	GAA Glu	TTA Leu	ATT Ile	ACT Thr 60	CTC Leu	TAT Tyr	CAG Gln	AGG Arg	192
CAC His 65	TTA Leu	TTG Leu	GAC Asp	GTT Val	GTA Val 70	GAC Asp	AAA Lys	GTT Val	GTT Val	ATA Ile 75	GAG Glu	GAC Asp	ACA Thr	TTG Leu	GTT Val 80	240
ATA Ile	CTC Leu	AAG Lys	CTT Leu	GCT Ala 85	AAT Asn	ATA Ile	TGT Cys	GGT Gly	AAA Lys 90	GCT Ala	тст Суз	ATG Met	AAG Lys	CTA Leu 95	TTG Leu	288
GAT Asp	AGA Arg	TGT Cys	AAA Lys 100	GAG Glu	ATT Ile	ATT Ile	GTC Val	AAG Lys 105	TCT Ser	AAT Asn	GTA Val	GAT Asp	ATG Met 110	GTT Val	AGT Ser	336
CTT Leu	GAA Glu	AAG Lys 115	TCA Ser	TTG Leu	CCG Pro	GAA Glu	GAG Glu 120	CTT Leu	GTT Val	AAA Lys	GAG Glu	ATA Ile 125	ATT Ile	GAT Asp	AGA Arg	384
CGT Arg	AAA Lys 130	GAG Glu	CTT Leu	GGT Gly	TTG Leu	GAG Glu 135	GTA Val	CCT Pro	AAA Lys	GTA Val	AAG Lys 140	AAA Lys	CAT His	GTC Val	TCG Ser	432
AAT Asn 145	GTA Val	CAT His	AAG Lys	GCA Ala	CTT Leu 150	GAC Asp	TCG Ser	GAT Asp	GAT Asp	ATT Ile 155	GAG Glu	TTA Leu	GTC Val	AAG Lys	TTG Leu 160	480
CTT Leu	TTG Leu	AAA Lys	GAG Glu	GAT Asp 165	CAC His	ACC Thr	AAT Asn	CTA Leu	GAT Asp 170	GAT Asp	GCG Ala	TGT Cys	GCT Ala	CTT Leu 175	CAT His	528
TTC Phe	GCT Ala	GTT Val	GCA Ala 180	TAT Tyr	TGC Cys	AAT Asn	GTG Val	AAG Lys 185	ACC Thr	GCA Ala	ACA Thr	GAT Asp	CTT Leu 190	TTA Leu	AAA Lys	576
CTT Leu	GAT Asp	CTT Leu 195	GCC Ala	GAT Asp	GTC Val	AAC Asn	CAT His 200	AGG Arg	AAT Asn	CCG Pro	AGG Arg	GGA Gly 205	TAT Tyr	ACG Thr	GTG Val	624
CTT Leu	CAT His 210	GTT Val	GCT Ala	GCG Ala	ATG Met	CGG Arg 215	AAG Lys	GAG Glu	CCA Pro	CAA Gln	TTG Leu 220	Ile	CTA Leu	TCT Ser	CTA Leu	672
TTG Leu 225	Glu	AAA Lys	GGT Gly	GCA Ala	AGT Ser 230	GCA Ala	TCA Ser	GAA Glu	GCA Ala	ACT Thr 235	TTG Leu	GAA Glu	GGT Gly	AGA Arg	ACC Thr 240	720
GCA Ala	CTC Leu	ATG Met	ATC Ile	GCA Ala 245	Lys	CAA Gln	GCC Ala	ACT Thr	ATG Met 250	Ala	GTT Val	GAA Glu	TGT Cys	AAT Asn 255	AAT Asn	768
ATC Ile	CCG Pro	GAG Glu	CAA Gln 260	Cys	AAG Lys	CAT His	TCT Ser	CTC Leu 265	Lys	GGC Gly	CGA Arg	CTA Leu	TGT Cys 270	Val	GAA Glu	816
ATA Ile	CTA Leu	GAG Glu 275	. Gln	GAA Glu	GAC Asp	AAA Lys	CGA Arg 280	Glu	. CAA . Gln	ATT Ile	CCT Pro	AGA Arg 285	GAT Asp	GTT Val	CCT Pro	864
CCC Pro	TCT Ser 290	Phe	GCA Ala	. GTG Val	GCG Ala	GCC Ala 295	Asp	GAA Glu	TTG Leu	AAG Lys	ATG Met 300	Thr	CTG Leu	CTC Leu	GAT Asp	912

CTT Leu 305	GAA Glu	AAT Asn	AGA Arg	GTT Val	GCA Ala 310	CTT Leu	GCT Ala	CAA Gln	CGT Arg	CTT Leu 315	TTT Phe	CCA Pro	ACG Thr	GAA Glu	GCA Ala 320	960
CAA Gln	GCT Ala	GCA Ala	ATG Met	GAG Glu 325	ATC Ile	GCC Ala	GAA Glu	ATG Met	AAG Lys 330	GGA Gly	ACA Thr	TGT Cys	GAG Glu	TTC Phe 335	ATA Ile	1008
GTG Val	ACT Thr	AGC Ser	CTC Leu 340	GAG Glu	CCT Pro	GAC Asp	CGT Arg	CTC Leu 345	ACT Thr	GGT Gly	ACG Thr	AAG Lys	AGA Arg 350	ACA Thr	TCA Ser	1056
CCG Pro	GGT Gly	GTA Val 355	AAG Lys	ATA Ile	GCA Ala	CCT Pro	TTC Phe 360	AGA Arg	ATC Ile	CTA Leu	GAA Glu	GAG Glu 365	CAT His	CAA Gln	AGT Ser	1104
AGA Arg	CTA Leu 370	AAA Lys	GCG Ala	CTT Leu	TCT Ser	AAA Lys 375	ACC Thr	GTG Val	GAA Glu	CTC Leu	GGG Gly 380	AAA Lys	CGA Arg	TTC Phe	TTC Phe	1152
CCG Pro 385	CGC Arg	TGT Cys	TCG Ser	GCA Ala	GTG Val 390	CTC Leu	GAC Asp	CAG Gln	ATT Ile	ATG Met 395	AAC Asn	TGT Cys	TGA *			1194

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 398 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val 1 10 15

Arg Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys 20 25 30

His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr 35 40 45

Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg 50 55 60

His Leu Leu Asp Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val 65 70 75 80

Ile Leu Lys Leu Ala As<br/>n Ile Cys Gly Lys Ala Cys Met Lys Leu Leu 85 90 95

Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser 100 105 110

Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg 115 120 125

Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser 130 135 140

Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu 145 150 155 160 Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His
165 170 175

Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Lys 180 185 190

Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val 195 200 205

Leu His Val Ala Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu 210 215 220

Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr 225 230 235 240

Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn 245 250 255

Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu 260 265 270

Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro 275 280 285

Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp 290 295 300

Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala 305 310 315 320

Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile 325 330 335

Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser 340 345 350

Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser 355 360 365

Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe 370 380

Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met Asn Cys \* 385 390 395

- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 786 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  - (2, 222222
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..786
  - (D) OTHER INFORMATION: /product= "Altered form of NIM1" /note= "Ankyrin domains of NIM1."
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATG Met 1	GAC Asp	TCC Ser	AAC Asn	AAC Asn 5	ACC Thr	GCC Ala	GCC Ala	GTG Val	AAG Lys 10	CTC Leu	GAG Glu	CTT Leu	AAG Lys	GAG Glu 15	ATT Ile	48
GCC Ala	AAG Lys	GAT Asp	TAC Tyr 20	GAA Glu	GTC Val	GGT Gly	TTC Phe	GAT Asp 25	TCG Ser	GTT Val	GTG Val	ACT Thr	GTT Val 30	TTG Leu	GCT Ala	96
TAT Tyr	GTT Val	TAC Tyr 35	AGC Ser	AGC Ser	AGA Arg	GTG Val	AGA Arg 40	CCG Pro	CCG Pro	CCT Pro	AAA Lys	GGA Gly 45	GTT Val	TCT Ser	GAA Glu	144
TGC Cys	GCA Ala 50	GAC Asp	GAG Glu	AAT Asn	TGC Cys	TGC Cys 55	CAC His	GTG Val	GCT Ala	TGC Cys	CGG Arg 60	CCG Pro	GCG Ala	GTG Val	GAT Asp	192
TTC Phe 65	ATG Met	TTG Leu	GAG Glu	GTT Val	CTC Leu 70	TAT Tyr	TTG Leu	GCT Ala	TTC Phe	ATC Ile 75	TTC Phe	AAG Lys	ATC Ile	CCT Pro	GAA Glu 80	240
TTA Leu	ATT Ile	ACT Thr	CTC Leu	TAT Tyr 85	CAG Gln	AGG Arg	CAC His	TTA Leu	TTG Leu 90	GAC Asp	GTT Val	GTA Val	GAC Asp	AAA Lys 95	GTT Val	288
GTT Val	ATA Ile	GAG Glu	GAC Asp 100	ACA Thr	TTG Leu	GTT Val	ATA Ile	CTC Leu 105	AAG Lys	CTT Leu	GCT Ala	AAT Asn	ATA Ile 110	TGT Cys	GGT Gly	336
AAA Lys	GCT Ala	TGT Cys 115	ATG Met	AAG Lys	CTA Leu	TTG Leu	GAT Asp 120	AGA Arg	TGT Cys	AAA Lys	GAG Glu	ATT Ile 125	ATT Ile	GTC Val	AAG Lys	384
TCT Ser	AAT Asn 130	GTA Val	GAT Asp	ATG Met	GTT Val	AGT Ser 135	CTT Leu	GAA Glu	AAG Lys	TCA Ser	TTG Leu 140	CCG Pro	GAA Glu	GAG Glu	CTT Leu	432
GTT Val 145	AAA Lys	GAG Glu	ATA Ile	ATT Ile	GAT Asp 150	AGA Arg	CGT Arg	AAA Lys	GAG Glu	CTT Leu 155	GGT Gly	TTG Leu	GAG Glu	GTA Val	CCT Pro 160	480
AAA Lys	GTA Val	AAG Lys	AAA Lys	CAT His 165	Val	TCG Ser	AAT Asn	GTA Val	CAT His 170	AAG Lys	GCA Ala	CTT Leu	GAC Asp	TCG Ser 175	GAT Asp	528
GAT Asp	ATT Ile	GAG Glu	TTA Leu 180	GTC Val	AAG Lys	TTG Leu	CTT Leu	TTG Leu 185	. Lys	GAG Glu	GAT Asp	CAC His	ACC Thr 190	Asn	CTA Leu	576
GAT Asp	GAT Asp	GCG Ala 195	. Суз	GCT Ala	CTT Leu	CAT His	TTC Phe 200	Ala	GTT Val	GCA Ala	TAT Tyr	TGC Cys 205	Asn	GTG Val	AAG Lys	624
ACC Thr	GCA Ala 210	Thr	GAT Asp	CTT Leu	TTA Leu	. AAA . Lys 215	Leu	GAT Asp	CTT Leu	GCC Ala	GAT Asp 220	Val	: AAC . Asn	CAT His	AGG Arg	672
AAT Asn 225	Pro	AGG Arg	GGA Gly	TAT Tyr	ACG Thr 230	· Val	CTT Leu	CAT His	GTT Val	GCT Ala 235	Ala	ATG Met	G CGG Arg	AAG Lys	GAG Glu 240	720
CCA Pro	CAA Gln	TTC Lev	ATA	CTA Leu 245	ı Ser	CTA	TTG Lev	GA <i>A</i> Glu	A AAA 1 Lys 250	Gly	GCA Ala	AGT Ser	GCA Ala	A TCA Ser 255	A GAA Glu	768

# GCA ACT TTG GAA GGT TGA Ala Thr Leu Glu Gly \*

- (2) INFORMATION FOR SEQ ID NO:16:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile 1 5 15

Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala 20 25 30

Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu 35 40 45

Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp 50 55 60

Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu 65 70 75 80

Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val 85 90 95

Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly 100 105 110

Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys 115 120 125

Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu 130 135 140

Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro 145 150 155 160

Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp 165 170 175

Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu 180 185 190

Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys 195 200 205

Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg 210 215 220

Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu 225 230 235

Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu 245 250 255

Ala Thr Leu Glu Gly \*

- (2) INFORMATION FOR SEQ ID NO:17:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val 1 5 10 15

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala 20 25 30

Val His Tyr Ala Val Gln His Cys Asn 35 40

- (2) INFORMATION FOR SEQ ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 38 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Thr Gly Lys Thr Ala Leu His Leu Ala Ala Glu Met Val Ser Pro 1 10 15

Asp Met Val Ser Val Leu Leu Asp His His Ala Asp Xaa Asn Phe Arg 20 25 30

Thr Xaa Asp Gly Val Thr 35

- (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala

Val His Tyr Ala Val Gln His Cys Asn 40

- (2) INFORMATION FOR SEQ ID NO:20:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 27 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Arg Pro Asp Ser Lys Thr Ala Leu His Leu Ala Ala Glu Met Val

Ser Pro Asp Met Val Ser Val Leu Leu Asp Gln 20

- (2) INFORMATION FOR SEQ ID NO:21:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala

Val His Tyr Ala Val Gln His Cys Asn

- (2) INFORMATION FOR SEQ ID NO:22:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 27 amino acids

    - (B) TYPE: amino acid (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Arg Pro Asp Ser Lys Thr Ala Leu His Leu Ala Ala Glu Met Val 15

Ser Pro Asp Met Val Ser Val Leu Leu Asp Gln

- (2) INFORMATION FOR SEQ ID NO:23:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala 25

Val His Tyr Ala Val Gln His Cys Asn 35

- (2) INFORMATION FOR SEQ ID NO:24:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: peptide
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Thr Gly Lys Thr Ala Leu His Leu Ala Ala Glu Met Val Ser Pro 10

Asp Met Val

- (2) INFORMATION FOR SEQ ID NO:25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 35 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
CAACAGCTTC GAAGCCGTCT TTGACGCGCC GGATG	35
(2) INFORMATION FOR SEQ ID NO:26:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
CATCCGGCGC GTCAAAGACG GCTTCGAAGC TGTTG	35
(2) INFORMATION FOR SEQ ID NO:27:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 32 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
GGAATTCAAT GGATTCGGTT GTGACTGTTT TG	32
(2) INFORMATION FOR SEQ ID NO:28:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 28 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
GGAATTCTAC AAATCTGTAT ACCATTGG	28
(2) INFORMATION FOR SEO ID NO:29:	

(A) DESCRIPTION: /desc = "oligonucleotide"

(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:29:	
CGGAATTC	GA TCTCTTTAAT TTGTGAATTT C	31
(2) INFO	RMATION FOR SEQ ID NO:30:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GGAATTCT	CA ACAGTTCATA ATCTGGTCG	29
(2) INFO	RMATION FOR SEQ ID NO:31:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 31 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:31:	
GGAATTCA	AT GGACTCCAAC AACACCGCCG C	31
(2) INFO	RMATION FOR SEQ ID NO:32:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGAATTCTCA ACCTTCCAAA GTTGCTTCTG ATG